

# Sven Nahnsen

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

3,558  
citations

304743

22  
h-index

289244

40  
g-index

51  
all docs

51  
docs citations

51  
times ranked

6305  
citing authors

#	ARTICLE	IF	CITATIONS
1	The nf-core framework for community-curated bioinformatics pipelines. <i>Nature Biotechnology</i> , 2020, 38, 276-278.	17.5	963
2	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
3	Swarm Learning for decentralized and confidential clinical machine learning. <i>Nature</i> , 2021, 594, 265-270.	27.8	375
4	Tools for Label-free Peptide Quantification. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 549-556.	3.8	198
5	Sustainable data analysis with Snakemake. <i>F1000Research</i> , 2021, 10, 33.	1.6	188
6	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 1628-1644.	3.7	146
7	Interpretations of Environmental Microbial Community Studies Are Biased by the Selected 16S rRNA (Gene) Amplicon Sequencing Pipeline. <i>Frontiers in Microbiology</i> , 2020, 11, 550420.	3.5	113
8	Multi-omics discovery of exome-derived neoantigens in hepatocellular carcinoma. <i>Genome Medicine</i> , 2019, 11, 28.	8.2	107
9	Suppression of Casein Kinase 1 $\alpha$ in Melanoma Cells Induces a Switch in $\beta$ -Catenin Signaling to Promote Metastasis. <i>Cancer Research</i> , 2010, 70, 6999-7009.	0.9	77
10	Personalized peptide vaccine-induced immune response associated with long-term survival of a metastatic cholangiocarcinoma patient. <i>Journal of Hepatology</i> , 2016, 65, 849-855.	3.7	75
11	Transcriptome Profiling Identifies TIGIT as a Marker of T $\alpha$ Cell Exhaustion in Liver Cancer. <i>Hepatology</i> , 2021, 73, 1399-1418.	7.3	61
12	Downregulation of TGR5 (GPBAR1) in biliary epithelial cells contributes to the pathogenesis of sclerosing cholangitis. <i>Journal of Hepatology</i> , 2021, 75, 634-646.	3.7	51
13	Clinical and Genetic Tumor Characteristics of Responding and Non-Responding Patients to PD-1 Inhibition in Hepatocellular Carcinoma. <i>Cancers</i> , 2020, 12, 3830.	3.7	47
14	Probabilistic Consensus Scoring Improves Tandem Mass Spectrometry Peptide Identification. <i>Journal of Proteome Research</i> , 2011, 10, 3332-3343.	3.7	45
15	ODG!: understanding pangenome graphs. <i>Bioinformatics</i> , 2022, 38, 3319-3326.	4.1	44
16	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42
17	Specific Induction of Double Negative B Cells During Protective and Pathogenic Immune Responses. <i>Frontiers in Immunology</i> , 2020, 11, 606338.	4.8	42
18	Optimal de novo Design of MRM Experiments for Rapid Assay Development in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 2696-2704.	3.7	40

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19	Measles Virus-Based Treatments Trigger a Pro-inflammatory Cascade and a Distinctive Immunopeptidome in Glioblastoma. <i>Molecular Therapy - Oncolytics</i> , 2019, 12, 147-161.	4.4	38
20	Mass spectrometry at the interface of proteomics and genomics. <i>Molecular BioSystems</i> , 2011, 7, 284-291.	2.9	36
21	Ring1b-dependent epigenetic remodelling is an essential prerequisite for pancreatic carcinogenesis. <i>Gut</i> , 2019, 68, 2007-2018.	12.1	27
22	The impact of winter feed type on intestinal microbiota and parasites in honey bees. <i>Apidologie</i> , 2018, 49, 252-264.	2.0	25
23	nf-core/mag: a best-practice pipeline for metagenome hybrid assembly and binning. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac007.	3.2	24
24	Challenges of big data integration in the life sciences. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 6791-6800.	3.7	22
25	Genetic evolution of <i>in situ</i> follicular neoplasia to aggressive B-cell lymphoma of germinal center subtype. <i>Haematologica</i> , 2021, 106, 2673-2681.	3.5	21
26	Mass-Spectrometry-Based Proteomics Reveals Organ-Specific Expression Patterns To Be Used as Forensic Evidence. <i>Journal of Proteome Research</i> , 2016, 15, 182-192.	3.7	19
27	qPortal: A platform for data-driven biomedical research. <i>PLoS ONE</i> , 2018, 13, e0191603.	2.5	18
28	A data management infrastructure for the integration of imaging and omics data in life sciences. <i>BMC Bioinformatics</i> , 2022, 23, 61.	2.6	18
29	Ten simple rules for providing effective bioinformatics research support. <i>PLoS Computational Biology</i> , 2020, 16, e1007531.	3.2	15
30	Platforms and Pipelines for Proteomics Data Analysis and Management. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 203-215.	1.6	14
31	Contribution of mTOR and PTEN to Radioresistance in Sporadic and NF2-Associated Vestibular Schwannomas: A Microarray and Pathway Analysis. <i>Cancers</i> , 2020, 12, 177.	3.7	13
32	Potent Antitumor Activity of Liposomal Irinotecan in an Organoid- and CRISPR-Cas9-Based Murine Model of Gallbladder Cancer. <i>Cancers</i> , 2019, 11, 1904.	3.7	11
33	In silico design of targeted SRM-based experiments. <i>BMC Bioinformatics</i> , 2012, 13, S8.	2.6	9
34	Absence of Non-Canonical, Inhibitory MYD88 Splice Variants in B Cell Lymphomas Correlates With Sustained NF- $\kappa$ B Signaling. <i>Frontiers in Immunology</i> , 2021, 12, 616451.	4.8	8
35	Proteome and phosphoproteome analysis of commensally induced dendritic cell maturation states. <i>Journal of Proteomics</i> , 2018, 180, 11-24.	2.4	6
36	PTMeta: Increasing identification rates of modified peptides using modification prescanning and meta-analysis. <i>Proteomics</i> , 2013, 13, 1042-1051.	2.2	5

#	ARTICLE	IF	CITATIONS
37	The Draft Whole-Genome Sequence of the Antibiotic Producer <i>Empedobacter haloabium</i> ATCC 31962 Provides Indications for Its Taxonomic Reclassification. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
38	Intuitive Web-Based Experimental Design for High-Throughput Biomedical Data. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	3
39	Experimental glioma with high bHLH expression harbor increased replicative stress and are sensitive toward ATR inhibition. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa115.	0.7	2
40	Interactive Visualization for Large-Scale Multi-factorial Research Designs. <i>Lecture Notes in Computer Science</i> , 2019, , 75-84.	1.3	1
41	CSIG-15. INHIBITION OF THE bHLH TRANSCRIPTIONAL NETWORKS BY A MUTATED E47 PROTEIN LEADS TO A STRONG ANTI-GLIOMA ACTIVITY IN VITRO AND IN VIVO. <i>Neuro-Oncology</i> , 2019, 21, vi47-vi47.	1.2	0
42	Interdisciplinary management of central nervous system metastasis and neoplastic meningitis: recent developments and future perspectives. <i>Journal of Cancer Metastasis and Treatment</i> , 2016, 2, 163.	0.8	0